

SEQUENCE LISTING

<110> Shorrosh, Basil S.
DeBonte, Lorin R.

<120> PLANTS CONTAINING A CYTOSOLIC ACETYL
COA-CARBOXYLASE

<130> 07148-094001

<150> US 60/198,794

<151> 2000-04-20

<160> 12

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<223> primer for PCR

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Val Ala Gln Ala Asn Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ala
20 25 30

T00240-246660

gcc tca ttc cct gtt tca agg aag caa aac ctt gac atc act tcc att 144
 Ala Ser Phe Pro Val Ser Arg Lys Gln Asn Leu Asp Ile Thr Ser Ile
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gcc agc aac ggc gga aga gtg caa tgc atg cag gtg tgg cca cca att 192
 Ala Ser Asn Gly Gly Arg Val Gln Cys Met Gln Val Trp Pro Pro Ile
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 Asn Lys Lys Ser
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 Ala Ser Asn Gly Gly Arg Val Gln Cys Met Gln Val Trp Pro Pro Ile
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 Asn Lys Lys Ser
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 <212> DNA
 <213> Artificial Sequence

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F00240" 4245860

<212> DNA

<213> *Medicago sativa*

<220>

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agt agg cac cct gct act aca acc gaa gta gat gaa tac tgc aat gcc	96
Ser Arg His Pro Ala Thr Thr Thr Glu Val Asp Glu Tyr Cys Asn Ala	
20 25 30	
ctt gga gga aac aag ccg att cat agc ata ttg att gca aac aat gga	144
Leu Gly Gly Asn Lys Pro Ile His Ser Ile Leu Ile Ala Asn Asn Gly	
35 40 45	
atg gca gca gtc aag ttt ata cgt agt gtt agg agt tgg gct tac gag	192
Met Ala Ala Val Lys Phe Ile Arg Ser Val Arg Ser Trp Ala Tyr Glu	
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aca ttt ggc acg gaa aaa gct atc ttg ttg gtt gcc atg gca act cca	240
Thr Phe Gly Thr Glu Lys Ala Ile Leu Leu Val Ala Met Ala Thr Pro	
65 70 75 80	
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Glu Asp Met Arg Ile Asn Ala Glu His Ile Arg Ile Ala Asp Gln Phe	
85 90 95	
gtg gaa gta cct ggt ggg acc aat aac aat aac tac gcc aat gtg cag	336
Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Gln	
100 105 110	
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Leu Ile Leu Glu Ile Ala Glu Ile Thr His Val Asp Ala Val Trp Pro	
115 120 125	
ggt tgg ggt cat gca tca gaa aat cct gag ctt cca gat gca tta aaa	432
Gly Trp Gly His Ala Ser Glu Asn Pro Glu Leu Pro Asp Ala Leu Lys	
130 135 140	
gca aag gga att gta ttc ctt gga cct cct gct ata tct atg gca gca	480
Ala Lys Gly Ile Val Phe Leu Gly Pro Pro Ala Ile Ser Met Ala Ala	
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Leu Gly Asp Lys Ile Gly Ser Ser Leu Ile Ala Gln Ala Ala Glu Val	
165 170 175	
cca acc ctt cca tgg agt ggt tct cat gtg aaa att cct cca gaa agt	576
Pro Thr Leu Pro Trp Ser Gly Ser His Val Lys Ile Pro Pro Glu Ser	
180 185 190	
gac ttg att act att cct gat gaa att tac cgt gca gca tgt gtt tat	624

F00240" 2455550

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Thr	Thr	Glu	Glu	Ala	Ile	Ala	Ser	Cys	Gln	Val	Val	Gly	Tyr	Pro	Ala		
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cat	aat	gat	gat	gag	gtt	agg	gca	ttg	ttc	aag	caa	gtt	caa	ggg	gaa	768	
His	Asn	Asp	Asp	Glu	Val	Arg	Ala	Leu	Phe	Lys	Gln	Val	Gln	Gly	Glu		
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Val	Pro	Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Val	Ala	Ser	Gln	Ser	Arg		
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cat	ctt	gaa	gtc	caa	ttg	att	tgc	gat	cag	cac	gga	aat	ttt	gca	gca	864	
His	Leu	Glu	Val	Gln	Leu	Ile	Cys	Asp	Gln	His	Gly	Asn	Phe	Ala	Ala		
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Leu	His	Ser	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln	Lys	Ile	Ile		
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gaa	cag	gcg	gct	aga	aga	tta	gct	aaa	tct	gta	aat	tat	gtg	ggg	gca	1008	
Glu	Gln	Ala	Ala	Arg	Arg	Leu	Ala	Lys	Ser	Val	Asn	Tyr	Val	Gly	Ala		
				325				330						335			
gct	acc	gtt	gag	tat	ctt	tat	agc	atg	gaa	act	ggc	gag	tac	tac	ttt	1056	
Ala	Thr	Val	Glu	Tyr	Leu	Tyr	Ser	Met	Glu	Thr	Gly	Glu	Tyr	Tyr	Phe		
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tta	gag	ttg	aac	ccc	cga	cta	cag	gtt	gag	cat	cct	gtt	act	gaa	tgg	1104	
Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	Val	Glu	His	Pro	Val	Thr	Glu	Trp		
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ata	gct	gag	ata	aat	ctg	cca	gca	gca	caa	gtt	gca	gtt	ggg	atg	ggc	1152	
Ile	Ala	Glu	Ile	Asn	Leu	Pro	Ala	Ala	Gln	Val	Ala	Val	Gly	Met	Gly		
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atc	cca	ctc	tgg	caa	att	cct	gag	att	agg	cgt	ttc	tat	ggg	atg	gaa	1200	
Ile	Pro	Leu	Trp	Gln	Ile	Pro	Glu	Ile	Arg	Arg	Phe	Tyr	Gly	Met	Glu		
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cat	ggg	ggg	gga	aat	gat	ggg	tgg	aag	aaa	aca	tca	gtg	tta	gct	acc	1248	
His	Gly	Gly	Gly	Asn	Asp	Gly	Trp	Lys	Lys	Thr	Ser	Val	Leu	Ala	Thr		
				405				410					415				
cct	ttt	gat	ttt	gac	gaa	gca	caa	tct	aca	aag	ccg	aaa	ggg	cat	tgt	1296	
Pro	Phe	Asp	Phe	Asp	Glu	Ala	Gln	Ser	Thr	Lys	Pro	Lys	Gly	His	Cys		

098947.04200

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tgg gct tat ttc tct gtt aag tcc gga gga gga att cat gaa ttc tca Trp Ala Tyr Phe Ser Val Lys Ser Gly Gly Gly Ile His Glu Phe Ser 465 470 475 480			1440
gat tct caa ttt gga cat gtt ttt gcg ttt gga gaa tct aga gct tta Asp Ser Gln Phe Gly His Val Phe Ala Phe Gly Glu Ser Arg Ala Leu 485 490 495			1488
gca att gca aat atg gta ctg ggg ttg aag gaa att caa att cga gga Ala Ile Ala Asn Met Val Leu Gly Leu Lys Glu Ile Gln Ile Arg Gly 500 505 510			1536
gaa att cgt acc aac gtt gat tac aca att gat ctt ctg aat gct tca Glu Ile Arg Thr Asn Val Asp Tyr Thr Ile Asp Leu Leu Asn Ala Ser 515 520 525			1584
gac tac aga gac aac aaa att cac aca gga tgg cta gac agt aga att Asp Tyr Arg Asp Asn Lys Ile His Thr Gly Trp Leu Asp Ser Arg Ile 530 535 540			1632
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gac tat gtt ggc tat ctt gaa aag ggg caa atc cct ccc aag cac att Asp Tyr Val Gly Tyr Leu Glu Lys Gly Gln Ile Pro Pro Lys His Ile 580 585 590			1776
tct ctt gtc cat tct caa gtt tct ttg agc att gaa gga agc aaa tac Ser Leu Val His Ser Gln Val Ser Leu Ser Ile Glu Gly Ser Lys Tyr 595 600 605			1824
acg att gac atg gta cga gga gga cct gga agt tac aaa ttg aaa ttg Thr Ile Asp Met Val Arg Gly Gly Pro Gly Ser Tyr Lys Leu Lys Leu 610 615 620			1872
aat caa tcg gag ata gaa gcg gag ata cac act tta cgt gat gga ggt Asn Gln Ser Glu Ile Glu Ala Glu Ile His Thr Leu Arg Asp Gly Gly 625 630 635 640			1920
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T00210" 446E86D

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cca tat gct gaa gtt gag gtc atg aag atg tgc atg cct ctt ctt tcc Pro Tyr Ala Glu Val Glu Val Met Lys Met Cys Met Pro Leu Leu Ser 705 710 715 720	2160
cct gct tct gga att att cat ttc aga atg gct gaa ggt caa gcc atg Pro Ala Ser Gly Ile Ile His Phe Arg Met Ala Glu Gly Gln Ala Met 725 730 735	2208
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cct act gca att tca ggt aaa gtt cat cag aaa tgt gca gca agc tta Pro Thr Ala Ile Ser Gly Lys Val His Gln Lys Cys Ala Ala Ser Leu 770 775 780	2352
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aaa gat ctt aga aac gag ttg gaa gct aaa tat aag gag ttc gaa att Lys Asp Leu Arg Asn Glu Leu Glu Ala Lys Tyr Lys Glu Phe Glu Ile 835 840 845	2544
att tca agc tcc caa act att gat ttc cct gcc aaa tta ttg aag gca Ile Ser Ser Ser Gln Thr Ile Asp Phe Pro Ala Lys Leu Leu Lys Ala 850 855 860	2592
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T00240" 246E860

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Gly	Gly	Arg	Glu	Ser	His	Ala	His	Lys	Ile	Val	Gln	Ser	Leu	Phe	Glu	
			900						905			910				
gag	tat	ctt	tca	gtt	gaa	gaa	cta	ttc	agt	gat	aat	ata	cag	gct	gat	2784
Glu	Tyr	Leu	Ser	Val	Glu	Glu	Leu	Phe	Ser	Asp	Asn	Ile	Gln	Ala	Asp	
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gta	att	gaa	cga	ctc	cgt	ctt	caa	tac	aag	aaa	gat	ttg	ttg	aag	att	2832
Val	Ile	Glu	Arg	Leu	Arg	Leu	Gln	Tyr	Lys	Lys	Asp	Leu	Leu	Lys	Ile	
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Val	Asp	Ile	Val	Leu	Ser	His	Gln	Gly	Val	Lys	Ser	Lys	Asn	Lys	Leu	
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Ile	Leu	Arg	Leu	Met	Asp	Lys	Leu	Val	Tyr	Pro	Asn	Pro	Ala	Ala	Tyr	
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Arg	Asp	Gln	Leu	Ile	Arg	Phe	Ser	Gln	Leu	Asn	His	Ile	Val	Tyr	Ser	
			980						985			990				
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Glu	Leu	Ala	Leu	Lys	Ala	Ser	Gln	Leu	Leu	Glu	Gln	Thr	Lys	Leu	Ser	
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gaa	ctt	cga	tcc	agc	att	gct	aga	agt	ctt	tct	gaa	cta	gaa	atg	ttt	3072
Glu	Leu	Arg	Ser	Ser	Ile	Ala	Arg	Ser	Leu	Ser	Glu	Leu	Glu	Met	Phe	
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acc	gag	gat	ggt	gaa	aat	att	gat	act	ccg	aag	agg	aag	agt	gcc	att	3120
Thr	Glu	Asp	Gly	Glu	Asn	Ile	Asp	Thr	Pro	Lys	Arg	Lys	Ser	Ala	Ile	
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aat	gac	aga	atg	gag	gac	ctt	gtg	agc	gct	cct	ttg	gct	gtt	gaa	gat	3168
Asn	Asp	Arg	Met	Glu	Asp	Leu	Val	Ser	Ala	Pro	Leu	Ala	Val	Glu	Asp	
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gcc	ctt	gtt	ggt	tta	ttt	gat	cac	agc	gat	cac	acc	ctt	caa	agg	aga	3216
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Val	Val	Glu	Thr	Tyr	Ile	Arg	Arg	Leu	Tyr	Gln	Pro	Tyr	Leu	Val	Lys	
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Asp	Ser	Ile	Arg	Met	Gln	Trp	His	Arg	Ser	Gly	Leu	Ile	Ala	Thr	Trp	
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	1170					1175				1180						
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1185					1190				1195					1200		
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				1205					1210					1215		
tcc Ser	ata Ile	ata Ile	cat His	gct Ala	gca Ala	ggg Gly	gtt Val	gga Gly	gat Asp	att Ile	agc Ser	tgt Cys	atc Ile	ata Ile	cag Gln	3696
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agg Arg	gat Asp	gaa Glu	ggg Gly	cgt Arg	gct Ala	cca Pro	atg Met	agg Arg	cat His	tcc Ser	ttt Phe	cac His	tgg Trp	tca Ser	tct Ser	3744
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gaa Glu	aag Lys	cta Leu	tat Tyr	tat Tyr	gta Val	gag Glu	gaa Glu	cca Pro	ttg Leu	ttg Leu	ctc Leu	cat His	ctt Leu	gaa Glu	cct Pro	3792
	1250					1255					1260					
ccc Pro	cta Leu	tcc Ser	att Ile	tat Tyr	ctt Leu	gaa Glu	ctg Leu	gac Asp	aag Lys	ctt Leu	aag Lys	tgc Cys	tat Tyr	gaa Glu	aat Asn	3840
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att Ile	cgc Arg	tat Tyr	aca Thr	cca Pro	tcc Ser	cga Arg	gat Asp	cgt Arg	caa Gln	tgg Trp	cac His	ctc Leu	tac Tyr	aca Thr	gtt Val	3888
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gat Asp	gca Ala	gaa Glu	acg Thr	tcc Ser	cgt Arg	acc Thr	caa Gln	ttg Leu	gct Ala	atg Met	tct Ser	tat Tyr	act Thr	tca Ser	agg Arg	4032

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Ser Ile Phe Arg Ser Leu Met Gly Ala Met Glu Glu Leu Glu Leu Asn			
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Ser His Asn Thr Thr Ile Lys Ser Glu His Ala His Met Tyr Leu Tyr			
1365	1370		1375
atc ata cgc gag cag caa ata gat gat ctt gtg cct tat tcc aag aaa			4176
Ile Ile Arg Glu Gln Gln Ile Asp Asp Leu Val Pro Tyr Ser Lys Lys			
1380	1385		1390
att aac ata gaa gct ggc caa gaa gaa aca aca gtt gag gca atc ttg			4224
Ile Asn Ile Glu Ala Gly Gln Glu Glu Thr Thr Val Glu Ala Ile Leu			
1395	1400		1405
gaa gaa ctg gca cag gaa atc cat tcc tct gtt ggt gta aga atg cac			4272
Glu Glu Leu Ala Gln Glu Ile His Ser Ser Val Gly Val Arg Met His			
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aga tta ggc gtt ttc gtg tgg gaa atc aag ctc tgg att aca gca tgt			4320
Arg Leu Gly Val Phe Val Trp Glu Ile Lys Leu Trp Ile Thr Ala Cys			
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gga cag gca aat ggt gct tgg agg gtc att gta aac aat gtg act ggt			4368
Gly Gln Ala Asn Gly Ala Trp Arg Val Ile Val Asn Asn Val Thr Gly			
1445	1450		1455
cat aca tgc act gta cat ata tat cga gag atg gag gat gcc acc act			4416
His Thr Cys Thr Val His Ile Tyr Arg Glu Met Glu Asp Ala Thr Thr			
1460	1465		1470
cat aaa gtg gtc tac agt tca gtc act gta aag ggt ccg ttg cat ggt			4464
His Lys Val Val Tyr Ser Ser Val Thr Val Lys Gly Pro Leu His Gly			
1475	1480		1485
gta ccg gtg aat gaa aac tat caa cct ttg gga ggt att gac cga aaa			4512
Val Pro Val Asn Glu Asn Tyr Gln Pro Leu Gly Gly Ile Asp Arg Lys			
1490	1495		1500
cgt ctt gca gcg aga aag aac agc acc aca tac tgc tat gat ttc ccc			4560
Arg Leu Ala Ala Arg Lys Asn Ser Thr Thr Tyr Cys Tyr Asp Phe Pro			
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ctt gca ttt caa aca tcc ttg gaa cag tcc tgg tca ata cag cag aca			4608
Leu Ala Phe Gln Thr Ser Leu Glu Gln Ser Trp Ser Ile Gln Gln Thr			
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gga att caa aga gct aat gat aag gat ctc cta aaa gta aca gag ctt			4656
Gly Ile Gln Arg Ala Asn Asp Lys Asp Leu Leu Lys Val Thr Glu Leu			
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Lys Phe Ser Glu Lys Ala Gly Ser Trp Gly Thr Ser Leu Val Pro Ala			
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T00240 246880

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Ile Met Ala Thr Asn Gly Val Val His Leu Thr Val Ser Asp Asp Leu	
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Glu Val Glu Tyr Leu Pro Glu Asn Ser Cys Asp Pro Arg Ala Ala Ile	
1845 1850 1855	
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Ser Gly Thr Leu Asp Val Asn Gly Lys Trp Leu Gly Gly Ile Phe Asp	
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Lys Asp Ser Phe Val Glu Thr Leu Glu Gly Trp Ala Arg Thr Val Val	
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Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro Val Gly Ile Val Ala Val	
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Asp Ser His Glu Arg Val Val Pro Gln Ala Gly Gln Val Trp Phe Pro	
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Asp Ser Ala Thr Lys Thr Ala Gln Ala Ile Leu Asp Phe Asn Arg Glu	
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Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln Ala Gly Ser Thr Ile Val	
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Leu	Leu	Glu	Cys	Met	Arg	Arg	Leu	Asp	Gln	Gln	Leu	Ile	Asn	Leu	Lys		
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20

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 10
 catcaggaat agtaatcaag tca

23

<210> 11
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> representative construct (3' end)

<400> 11
 ccttttataa aaaaaaaaaa aagaattcct gcagcccggg ggatcc

46

<210> 12
 <211> 46
 <212> DNA
 <213> Artificial Sequence

T00240 462860

<220>

<223> representative construct (3' end)

<400> 12

ccttttataa aaaaaaaaaa aagaattcct gcagcccggg ggatcc

46

T00210" 445E360